PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/487,550*

DATE: 10/10/97
TIME: 08:46:18

INPUT SET: S12522.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
1                                   SEQUENCE LISTING
2
3   (1)     General Information:
4
5       (i) APPLICANT: Anderson, Darrell R.
6
7      (ii) TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
8               TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
9               PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
10              IMMUNOSUPPRESANTS"
11
12    (iii) NUMBER OF SEQUENCES: 12
13
14     (iv) CORRESPONDENCE ADDRESS:
15              (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
16              (B) STREET: 699 Prince Street
17              (C) CITY: Alexandria
18              (D) STATE: VA
19              (E) COUNTRY: USA
20              (F) ZIP: 22314
21
22      (v) COMPUTER READABLE FORM:
23              (A) MEDIUM TYPE: Floppy disk
24              (B) COMPUTER: IBM PC compatible
25              (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26              (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28     (vi) CURRENT APPLICATION DATA:
29              (A) APPLICATION NUMBER: US 08/487,550
30              (B) FILING DATE: 07-JUN-1995
31              (C) CLASSIFICATION:
32
33   (viii) ATTORNEY/AGENT INFORMATION:
34              (A) NAME: Teskin, Robin L.
35              (B) REGISTRATION NUMBER: 35,030
36              (C) REFERENCE/DOCKET NUMBER: 012712-131
37
38     (ix) TELECOMMUNICATION INFORMATION:
39              (A) TELEPHONE: 703-836-6620
40              (B) TELEFAX: 703-836-2021
41
42
43   (2) INFORMATION FOR SEQ ID NO:1:
44
45       (i) SEQUENCE CHARACTERISTICS:
46              (A) LENGTH: 705 base pairs
```

```
47           (B) TYPE: nucleic acid
48           (C) STRANDEDNESS: Not Relevant
49           (D) TOPOLOGY: linear
50
51       (ii) MOLECULE TYPE: peptide
52
53
54       (ix) FEATURE:
55           (A) NAME/KEY: CDS
56           (B) LOCATION: 1..705
57
58       (ix) FEATURE:
59           (A) NAME/KEY: mat_peptide
60           (B) LOCATION: 1..705
61
62
63       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
64
65   ATG AGG GTC CCC GCT CAG CTC CTG GGG CTC CTG CTG CTC TGG CTC CCA        48
66   Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro
67    1               5                  10                  15
68
69   GGT GCA CGA TGT GCC TAT GAA CTG ACT CAG CCA CCC TCG GTG TCA GTG        96
70   Gly Ala Arg Cys Ala Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val
71                20                  25                  30
72
73   TCC CCA GGA CAG ACG GCC AGG ATC ACC TGT GGG GGA GAC AAC AGT AGA       144
74   Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ser Arg
75                35                  40                  45
76
77   AAT GAA TAT GTC CAC TGG TAC CAG CAG AAG CCA GCG CGG GCC CCT ATA       192
78   Asn Glu Tyr Val His Trp Tyr Gln Gln Lys Pro Ala Arg Ala Pro Ile
79        50                  55                  60
80
81   CTG GTC ATC TAT GAT GAT AGT GAC CGG CCC TCA GGG ATC CCT GAG CGA       240
82   Leu Val Ile Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg
83    65                  70                  75                  80
84
85   TTC TCT GGC TCC AAA TCA GGG AAC ACC GCC ACC CTG ACC ATC AAC GGG       288
86   Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr Leu Thr Ile Asn Gly
87                85                  90                  95
88
89   GTC GAG GCC GGG GAT GAG GCT GAC TAT TAC TGT CAG GTG TGG GAC AGG       336
90   Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg
91                100                 105                 110
92
93   GCT AGT GAT CAT CCG GTC TTC GGA GGA GGG ACC CGG GTG ACC GTC CTA       384
94   Ala Ser Asp His Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu
95                115                 120                 125
96
97   GGT CAG CCC AAG GCT GCC CCC TCG GTC ACT CTG TTC CCG CCC TCC TCT       432
98   Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
99        130                 135                 140
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INPUT SET: S12522.raw

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101  GAG GAG CTT CAA GCC AAC AAG GCC ACA CTG GTG TGT CTC ATA AGT GAC        480
102  Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
103  145                 150                 155                 160
104
105  TTC TAC CCG GGA GCC GTG ACA GTG GCC TGG AAG GCA GAT AGC AGC CCC        528
106  Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
107                  165                 170                 175
108
109  GTC AAG GCG GGA GTG GAG ACC ACC ACA CCC TCC AAA CAA AGC AAC AAC        576
110  Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
111                  180                 185                 190
112
113  AAG TAC GCG GCC AGC AGC TAC CTG AGC CTG ACG CCT GAG CAG TGG AAG        624
114  Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
115              195                 200                 205
116
117  TCC CAC AGA AGC TAC AGC TGC CAG GTC ACG CAT GAA GGG AGC ACC GTG        672
118  Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
119      210                 215                 220
120
121  GAG AAG ACA GTG GCC CCT ACA GAA TGT TCA TGA                           705
122  Glu Lys Thr Val Ala Pro Thr Glu Cys Ser  *
123  225                 230                 235
124
125
126  (2) INFORMATION FOR SEQ ID NO:2:
127
128          (i) SEQUENCE CHARACTERISTICS:
129              (A) LENGTH:  234 amino acids
130              (B) TYPE: amino acid
131              (D) TOPOLOGY: linear
132
133          (ii) MOLECULE TYPE: protein
134
135          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
136
137  Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro
138   1               5               10                  15
139
140  Gly Ala Arg Cys Ala Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val
141              20              25                  30
142
143  Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ser Arg
144              35              40                  45
145
146  Asn Glu Tyr Val His Trp Tyr Gln Gln Lys Pro Ala Arg Ala Pro Ile
147       50              55                  60
148
149  Leu Val Ile Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg
150   65              70                  75                  80
151
152  Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr Leu Thr Ile Asn Gly
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INPUT SET: S12522.raw

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153                         85                   90                        95
154
155     Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg
156             100               105               110
157
158     Ala Ser Asp His Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu
159         .    115               120               125
160
161     Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
162         130               135               140
163
164     Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
165     145               150               155               160
166
167     Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
168             165               170               175
169
170     Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
171             180               185               190
172
173     Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
174             195               200               205
175
176     Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
177         210               215               220
178
179     Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
180     225               230               235
181
182     (2) INFORMATION FOR SEQ ID NO:3:
183
184         (i) SEQUENCE CHARACTERISTICS:
185             (A) LENGTH: 1431 base pairs
186             (B) TYPE: nucleic acid
187             (C) STRANDEDNESS: Not Relevant
188             (D) TOPOLOGY: linear
189
190         (ii) MOLECULE TYPE: peptide
191
192
193         (ix) FEATURE:
194             (A) NAME/KEY: CDS
195             (B) LOCATION: 1..1431
196
197         (ix) FEATURE:
198             (A) NAME/KEY: mat_peptide
199             (B) LOCATION: 1..1431
200
201
202         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
203
204     ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCT CCC AGA TGG       48
205     Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/487,550*

INPUT SET: S12522.raw

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206      1               5               10              15
207
208   GTC CTG TCC CAG GTG AAG CTG CAG CAG TGG GGC GAA GGA CTT CTG CAG        96
209   Val Leu Ser Gln Val Lys Leu Gln Gln Trp Gly Glu Gly Leu Leu Gln
210                    20               25              30
211
212   CCT TCG GAG ACC CTG TCC CGC ACC TGC GTT GTC TCT GGT GGC TCC ATC       144
213   Pro Ser Glu Thr Leu Ser Arg Thr Cys Val Val Ser Gly Gly Ser Ile
214                    35               40              45
215
216   AGC GGT TAC TAC TAC TGG ACC TGG ATC CGC CAG ACC CCA GGG AGG GGA       192
217   Ser Gly Tyr Tyr Tyr Trp Thr Trp Ile Arg Gln Thr Pro Gly Arg Gly
218            50               55               60
219
220   CTG GAG TGG ATT GGC CAT ATT TAT GGT AAT GGT GCG ACC ACC AAC TAC       240
221   Leu Glu Trp Ile Gly His Ile Tyr Gly Asn Gly Ala Thr Thr Asn Tyr
222    65                70               75                80
223
224   AAT CCC TCC CTC AAG AGT CGA GTC ACC ATT TCA AAA GAC ACG TCC AAG       288
225   Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Thr Ser Lys
226                    85               90                 95
227
228   AAC CAG TTC TTC CTG AAC TTG AAT TCT GTG ACC GAC GCG GAC ACG GCC       336
229   Asn Gln Phe Phe Leu Asn Leu Asn Ser Val Thr Asp Ala Asp Thr Ala
230                    100              105             110
231
232   GTC TAT TAC TGT GCG AGA GGC CCT CGC CCT GAT TGC ACA ACC ATT TGT       384
233   Val Tyr Tyr Cys Ala Arg Gly Pro Arg Pro Asp Cys Thr Thr Ile Cys
234            115              120              125
235
236   TAT GGC GGC TGG GTC GAT GTC TGG GGC CCG GGA GAC CTG GTC ACC GTC       432
237   Tyr Gly Gly Trp Val Asp Val Trp Gly Pro Gly Asp Leu Val Thr Val
238            130              135              140
239
240   TCC TCA GCT AGC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC       480
241   Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
242   145              150              155             160
243
244   TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG       528
245   Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
246                    165              170             175
247
248   GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG       576
249   Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
250                    180              185             190
251
252   ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC       624
253   Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
254            195              200              205
255
256   TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC       672
257   Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
258            210              215              220
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/487,550*

INPUT SET: S12522.raw

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423	Stop Codon at end of sequence removed - no error	
562	Stop Codon at end of sequence removed - no error	
807	Stop Codon at end of sequence removed - no error	
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1190	Stop Codon at end of sequence removed - no error	